

Amendments to the Claims:

Please cancel claims 10 and 15 without prejudice or disclaimer, please amend claims 1, 3-9, 11 and 12 and please enter new claims 49-53 as set forth in the complete listing of the claims below. The listing hereafter replaces all prior versions and listings.

1 (currently amended). A method for identifying a subject at risk of melanoma, which comprises detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample from a human subject, wherein the polymorphic variation is detected in an intron of a region between about the position of rs1267618 and about the position of rs1639679 nucleotide sequence selected from the group consisting of

(a) ~~the nucleotide sequence of SEQ ID NO: 1;~~

(b) ~~a nucleotide sequence which encodes an amino acid sequence encoded by SEQ ID NO: 1;~~

(c) ~~a nucleotide sequence which encodes an amino acid sequence that is 90% or more identical to the amino acid sequence encoded by SEQ ID NO: 1;~~

(d) ~~a fragment of a nucleotide sequence of (a), (b), or (c); and wherein the nucleotide sequence contains a thymine at position 171429 of SEQ ID NO: 1;~~

whereby the presence of the one or more polymorphic variations is indicative of the subject being at risk of melanoma.

2 (original). The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3 (currently amended). The method of claim 1, wherein the one or more polymorphic variations ~~is detected at~~ comprises a polymorphic variation at a site ~~position the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1~~ selected from the group consisting of rs1639679, rs1267646, rs1267636, rs1639675,

rs1267649, rs1267609, rs1267625, rs1267601, rs1267606 and rs1267621 446311,  
138875, 132526, 128002, 118712, 98846, 98682, 87826, 80400, 76779, 68398 and 64547.

4 (currently amended). The method of claim 3, wherein the one or more a  
polymorphic variations comprises ~~is detected at a~~ rs1639679 polymorphic variation position  
~~446311 in SEQ ID NO:1.~~

5 (currently amended). The method of claim 3, wherein the one or more a  
polymorphic variations comprises ~~is detected at a~~ rs1267636 polymorphic variation position  
~~132526 in SEQ ID NO:1.~~

6 (currently amended). The method of claim 3, wherein the one or more a  
polymorphic variations comprises ~~is detected at a~~ rs1639675 polymorphic variation position  
~~128002 in SEQ ID NO:1.~~

7 (currently amended). The method of claim 3, wherein the one or more a  
polymorphic variations comprises ~~is detected at a~~ rs1267649 polymorphic variation position  
~~118712 in SEQ ID NO:1.~~

8 (currently amended). The method of claim 3, wherein the one or more a  
polymorphic variations comprises ~~is detected at a~~ rs1267609 polymorphic variation position  
~~98846 in SEQ ID NO:1.~~

9 (currently amended). The method of claim 3, wherein the one or more a  
polymorphic variations comprises ~~is detected at a~~ rs1267601 polymorphic variation position  
~~80400 in SEQ ID NO:1.~~

10 (cancelled).

11 (currently amended). The method of claim 3, wherein the one or more  
polymorphic variations comprises ~~is~~ the haplotype CTTG corresponding to rs1639679,

rs1267646, rs1267606 and rs1267621 positions 446311, 138875, 76779, and 68398, respectively, in ~~SEQ ID NO: 1~~.

12 (currently amended). The method of claim 3, wherein the one or more polymorphic variations comprises is the haplotype ATGA corresponding to rs1639679, rs1267646, rs1267606 and rs1267621 positions 446311, 138875, 76779, and 68398, respectively, in ~~SEQ ID NO: 1~~.

13 (original). The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

14 (previously presented). The method of claim 13, wherein the oligonucleotide is selected from the group consisting of GTAATGTTGAACTACAATTACCA (SEQ ID NO: 45); GAAACAGGCTTCAATTCATCTT (SEQ ID NO: 46); ACATAGAGGCAGGACTGTCA (SEQ ID NO: 47); ATTAGGACATGGCTGAGATATTCA (SEQ ID NO: 48); GGACTCTGCTTATTCTACCCA (SEQ ID NO: 49); AGAGATTGTGCTTCCCAAATC (SEQ ID NO: 50); GAATTAGTGAACCTCTGGAAAGT (SEQ ID NO: 51); GAAATATGTTTGGAAAATTGTTCT (SEQ ID NO: 52); CTACAAAGCAAGACAGGACTAA (SEQ ID NO: 53); CCAAGATAAGAATCTGTTTTACC (SEQ ID NO: 54); AATGTTCTGAATTTTCCAATAA (SEQ ID NO: 55); and TTATAATTTAGTGGGGAACAGAA (SEQ ID NO: 56).

15-48 (cancelled).

49 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267646 polymorphic variation.

50 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267625 polymorphic variation.

51 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267606 polymorphic variation.

52 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a rs1267621 polymorphic variation.

53 (new). The method of claim 3, wherein the one or more polymorphic variations comprises a polymorphic variation at a site selected from the group consisting of rs1267649, rs1267609 and rs1267601.